

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 5, 2001, 13:02:37 ; Search time 100.35 Seconds

(Without alignments)
486,503 Million cell updates/sec

Title: US-09-593-316-2

Perfect score: 2003

Sequence: 1 MNVKGKVLISMLVSTIVV.....IKLYKMSQIKYNNVNNV 369

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 13230527 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPITREML16:
1: SP_archaea:
2: SP_bacteria:
3: SP_fungi:
4: SP_human:
5: SP_invertebrate:
6: SP_mammal:
7: SP_mhc:
8: SP_orphanella:
9: SP_phase:
10: SP_plant:
11: SP_rodent:
12: SP_unclassified:
13: SP_vertebrate:
14: SP_virus:

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	1711.5	85.4	376	6 Q28855
2	677	33.8	274	4 Q90065
3	673	33.6	274	4 Q90068
4	673	33.6	295	4 Q15951
5	673	33.6	354	4 Q14490
6	671	33.5	274	4 Q90063
7	670	33.4	274	4 Q14758
8	670	33.4	274	4 Q90069
9	670	33.4	274	4 Q90181
10	667	33.3	421	6 Q9TSM2
11	667	33.3	421	6 Q9TSM2
12	665	33.2	274	4 Q90062
13	665	33.2	274	4 Q90062
14	664	33.2	274	4 Q90066
15	663	33.1	274	4 Q90065
16	662	33.1	274	4 Q90064
17	661	33.0	274	4 Q15512
18	660	33.0	274	6 Q9TSM3
19	660	33.0	274	6 Q18825

20	658	32.9	274	6 Q97549
21	656	32.8	348	11 Q9ET32
22	655	32.7	312	6 Q9ETN4
23	649	32.4	277	6 Q9TSM1
24	649	32.4	289	6 Q9TUP0
25	646	32.3	327	11 Q9EOW3
26	646	32.3	332	11 Q9EOW2
27	645.5	32.2	271	6 Q9TV74
28	643	32.1	348	6 Q9TUD9
29	639	31.9	347	4 Q90K15
30	629.5	31.4	262	6 Q9ETN3
31	628.5	31.4	309	6 Q97551
32	627	31.3	347	6 Q95158
33	612	30.6	364	6 Q77563
34	538.5	26.9	229	4 Q9NW01
35	537.5	26.8	229	4 Q99479
36	532.5	26.6	229	4 Q9NW02
37	489.5	24.4	209	6 Q9GM53
38	468.5	23.4	190	6 Q62752
39	468.5	23.4	190	6 Q62858
40	467.5	23.3	190	6 Q62751
41	467.5	23.3	190	6 Q62753
42	464.5	23.2	190	6 Q62749
43	464.5	23.2	190	6 Q62748
44	460.5	23.0	209	6 Q9GM54
45	450.5	22.5	186	6 Q62750

ALIGNMENTS

RESULT 1
ID Q28855 PRELIMINARY: PKT: 376 AA.
AC Q28855:
DT 01-FEB-1997 (TRENDEL, 02, (created))
DT 01-FEB-1997 (TRENDEL, 02, last sequence update)
DT 01-OCT-2000 (TRENDEL, 15, last annotation update)
DE ALPHA 1.3 GALACTOSYLTRANSFERASE.
OS PLYTHRINI (New world monkeys).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates.
OX NCBI-TaxID=9479;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9431837; PubMed=8054718;
RA Henion T.R., Macher B.A., Anuraki F., Gallili U.;
RT "Defining the minimal size of catalytically active primate alpha 1.3
RT galactosyltransferase: structure-function studies on the recombinant
RT truncated enzyme."
RL Glycobiology 4:193-201(1994).
DR EMBL: S71333; AAB31587.2; -;
SO SEQUENCE 376 AA; 44471 MW; 136490C0BE2FA2DF CRC64;

Query Match 85.4%; Score 1711.5; DB 6; Length 376;
Best local Similarity 83.0%; Pred. No. 4,1e+130;
Matches 313; Conservative 33; Mismatches 22; Indels 9; Gaps 4;

QY 1 MNVKGKVLISMLVSTIVVFMFVYINSPESSJFWINSPNPFVSSGSSQKQKMWTRWPN 60
DB 1 MNVKGKVLISMLVSTIVVFMFVYINSPESSJFWINSPNPFVSSGSSQKQKMWTRWPN 59
QY 61 NG---VOEHEHDEWEK---EORKE-DKSKLISDFNFKPEVVMIMAKAPVWMS 112
DB 60 NCHNHYOQEEFDIDKEGREGDEQKKEHTTEFLPMWINKKPEVMTYQKAPPVWMS 119
QY 113 TYNKAVLDIDYAAOKITVGLTFVAVGRYTEHYLEELTSANKPEKQGHVITYVWVWS 172
DB 120 TYNKAVLEENYAAOKITVGLTFVAVGRYTEHYLEELTSANKPEKQGHVITYVWVWS 179
QY 173 RMLPELGLPSKVFPEVKERERQGVSWRMKTIIEHVAHQKRVDFLCMDVQVQV 242
DB 172 RMLPELGLPSKVFPEVKERERQGVSWRMKTIIEHVAHQKRVDFLCMDVQVQV 242

DB 180 KAFVLEHLEHRSKFEVKEVKKRWMJHLSMMKKTIGHLLAHLEHVEPLRPMVWVQVQ 239
 QY 233 DEFEVLEHESVAOLJAMVYKAPDEFEVEERKESAAVIFEGCHPYHAAIFEGCPYQV 292
 DB 240 DEFEVLEHESVAOLJAMVYKAPDEFEVEERKESAAVIFEGCHPYHAAIFEGCPYQV 299
 QY 293 LNTLOTEFKGILLKOKKNOLEAGWHDHSHLNKPELKNKPKILLSEPCWQYHIGLPADIKL 352
 DB 300 LNTLOTEFKGILLKOKKNOLEAGWHDHSHLNKPELKNKPKILLSEPCWQYHIGLPADIKL 359
 QY 453 VKRSMQIKREYNNRVN 469
 DB 460 VKLSWQIKREYNNRVN 476

RESULT 2
 QY09065 PRELIMINARY PRT 274 AA.

AC QY09065
 DT 01 MAY 2000 (TREMbled, 13, Great old)
 DT 01 MAY 2000 (TREMbled, 13, last sequence update)
 DT 01 MAY 2000 (TREMbled, 13, last annotation update)
 DE C1S AB SPECIFIC ALPHA 1-3 N ACETYLGLUTAMINYL TRANSFERASE
 (FRAGMENT).
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catartini; Homidae; Homo.
 OX NCBI TaxID=9606;
 RN 111
 RP SEQUENCE FROM N.A.
 RA Yamamoto F.;
 RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DB EMBL: AF144428; AAD26576.1;
 DB EMBL: AF144427; AAD26580.1; J01NEO.
 KW Transferrase.
 FT NON_TER 1
 FT NON_TER 274
 FT SEQUENCE 274 AA: 31997 MW: 57866.275028E2055 CIRC64;

Query Match 33.8%; Score 677; DB 4; Length 274;
 Best Local Similarity 47.1%; Pred. No. 0.7e 47;
 Matches 129; Conservative 49; Mismatches 94; Indels 2; Gaps 2;

QY 95 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 154
 DB 1 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 59
 QY 155 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 214
 DB 60 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 119
 QY 215 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 274
 DB 120 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 179
 QY 275 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 334
 DB 180 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 359
 QY 335 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 367
 DB 240 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 274

RESULT 3
 QY09068 PRELIMINARY PRT 274 AA.
 AC QY09068
 DT 01 MAY 2000 (TREMbled, 13, Great old)
 DT 01 MAY 2000 (TREMbled, 13, last sequence update)

DT 01-MAY-2000 (TREMbled, 13, last annotation update)
 DE AL SPECIFIC ALPHA 1-3 N ACETYLGLUTAMINYL TRANSFERASE (FRAGMENT).
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catartini; Homidae; Homo.
 OX NCBI TaxID=9606;
 RN 111
 RP SEQUENCE FROM N.A.
 RA Yamamoto F.;
 RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 DB EMBL: AF144428; AAD26576.1;
 DB EMBL: AF144427; AAD26580.1; J01NEO.
 KW Transferrase.
 FT NON_TER 1
 FT NON_TER 274
 FT SEQUENCE 274 AA: 31977 MW: 71860.76048E2055 CIRC64;

Query Match 33.8%; Score 673; DB 4; Length 274;
 Best Local Similarity 46.7%; Pred. No. 1.4e 46;
 Matches 128; Conservative 49; Mismatches 95; Indels 2; Gaps 2;

QY 95 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 154
 DB 1 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 59
 QY 155 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 214
 DB 60 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 119
 QY 215 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 274
 DB 120 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 179
 QY 275 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 334
 DB 180 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 359
 QY 335 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 367
 DB 240 RFEVYIMJMKKAVVWVSTYNNRAVLDVYAKKILVGLTVFAWRYLEHLEHLSANK 274

RESULT 4
 QY09061 PRELIMINARY PRT 295 AA.
 AC QY09061
 DT 01-MAY-1996 (TREMbled, 01, Great old)
 DT 01-JAN-1999 (TREMbled, 09, last sequence update)
 DT 01-NOV-1999 (TREMbled, 12, last annotation update)
 DE HISTO-BLOOD GROUP A2 TRANSFERASE (FRAGMENT).
 GN ABO.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catartini; Homidae; Homo.
 OX NCBI TaxID=9606;
 RN 111
 RP SEQUENCE FROM N.A.
 RA MEDLINE 9239251; PubMed 1520422;
 RA Yamamoto F.; McNoll P.D.; Hakomori S.;
 RT Human histo-blood group A2 transferase coded by A2 allele, one of the
 RT A subtypes, is characterized by a single base deletion in the coding
 RT sequence, which results in an additional domain at the catalytic
 RT terminal."
 RT Biochem. Biophys. Res. Commun. 187:366-374 (1992).
 RN 121
 RP SEQUENCE FROM N.A.
 RA Yamamoto F.;
 RT Submitted (MAR 1999) to the EMBL/GenBank/DBJ databases.
 DB EMBL: S44054; AAB2167.1;

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DR EMBL: AF134442; AAC26577.1; "
OR EMBL: AF134421; AAC26577.1; JOINED.
KM Transferase.
FT NOE_TERM 1
SQ SEQUENCE 295 AA; 34194 MW; 0DA3B373906BF588 CMC64;

Query Match      34.6%; Score 673; DB 4; Length 295;
Best local Similarity 46.7%; Pred. No. 1,6e-46;
Matches 128; Conservatio 4%; Mismatches 95; Indels 2; Gaps 2;

QY 95 RPVEVTMTDMKAPVMEGTYGNRAVEDDYAKAKITVGTTVPFVAGRYIEHYLEPFLTSANK 154
   1 : 1 : | | | | | | | | : : : : | : | : | : | : | : | : | : | : |
Db 1 KKDVLIVPLMIAPIWEGTFFNIDLNEOPFRDNTIIGLTFAIKKYVA-LKLPLETAEK 59
   155 HPMGHAVTFVVMVDVSRLPLFLGPKLSKFVEVKPERRMQODSVMAKTIIGEHIYAH 214
       ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 60 HMGGHAYHYVFTDGLAAVRPTLATGTGQSLYLHVPAVKRMQDVSMRMEMISDFCER 119
       ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 215 IOREVDLFCHDVDGVFDDEESVFELTGESVALOQLAMWTAKADPEFTYEERKESAAYIPFG 274
       ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 120 FLSEEDYLVCMVIMEFEPFDHWSELTLPFLGIHQFGSSREAFTEERRPOSAAYIPKD 179
       ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 275 EGDEEVYHAALIGGTGYULNITGEFKILKKRKDDINQAMDHSHLNKPYLLNNPTKITL 334
       ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 180 EGDEYLGGFSGSVEUQRTRACHQLAMMDQANGIEAWHDESHNLNKYILIRKPTKVL 239
       ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
QY 335 SPEEYGDYH-LGIPADIKIWKSWTKFEYNVRN 367
       ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 240 SPETIMIDOLLQMPAVLKRLKTAPAKNHQAVERN 273
       ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 5
Q14490 PRELIMINARY; PRT; 354 AA.
AC Q14490.
DT 01-NOV-1995 (TREMBLrel_01_Created)
DI 01-NOV-1996 (TREMBLrel_01_Last sequence update)
DI 01-NOV-1999 (TREMBLrel_12_Last annotation update)
DE HISTO-BLOOD GROUP A TRANSFERASE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95118355; PubMed=7598760;
RA Bennett E.P., Steltjensen R., Clausen H., Weghuis D.O.,
RT *Genomic cloning of the human histo-blood group ABO locus.*;
RI Biochem. Biophys. Res. Commun. 206:318-325(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95298046; PubMed=7779106;
RA Bennett E.P., Steltjensen R., Clausen H., Weghuis D.O.,
RT *Genomic cloning of the human histo-blood group ABO locus.*;
RI Biochem. Biophys. Res. Commun. 211:347-347(1995).
RN [3]
RP SEQUENCE FROM N.A.
RA Yamamoto F.;
RT Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL: X84746; CAAS59233.1; JOINED.
DR EMBL: X84747; CAAS59233.1; JOINED.
DR EMBL: X84748; CAAS59233.1; JOINED.
DR EMBL: X84749; CAAS59233.1; JOINED.
DR EMBL: X84750; CAAS59233.1; JOINED.
DR EMBL: X84751; CAAS59233.1; JOINED.
DR EMBL: X84752; CAAS59233.1; JOINED.
DR EMBL: AF134413; AAD26573.1; -
OR Transferase.
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Seq	SEQUENCE	354 AA	40950 MW	G344EF584F177134 C8C64
Query Match		33.6%	Score 673	DB 4; Length 354;
Best Local Similarity		46.7%	Pred. No. 26-46;	
Matches 128;	Conservative 49;	Mismatches 95;	Indels 2;	Gaps 2;
QY	95	REPVATMDKAPRVWESTYKRAVLDDYAAKQITVGLITPAVAGKITEHYEEELTSANK	154	
DB	81	KKDYLVVPLALPIWSEPTFNIDINQFRLONTIGLITPAIKKYVA-FKLPLEAK	139	
QY	155	HEMVGHRYFYVMVDVSRMPLIELGPKSKFVEFKEREDRQVSNRMKILCEHVAH	214	
DB	140	HEMVGHRYHYFTDQLAAVPRVTLGTGQSLVLEPRAYKRDQVSHKIMELSPCTEK	199	
QY	215	IQREVDPLFCMDVDFODEPGEFTIGESVAQLQMWYKADPEFTYERKKESAAVIFEG	274	
DB	200	FLSEVDYLVCVDVDEPFDHVGVELLTPLFTLHPGFGSSSEATFYERPRQVAYIKD	256	
QY	275	EGDFYYHAALFEGTIPQVINITQESFKGLIKDKKDIFQAMQDSEHLNKFTLANKPTKL	334	
DB	260	EGDFYYLGGFGGSGVQEVQRLTRACHQAMVVDQANGIAVWHDSEHLNKYLLRHKPTKL	319	
QY	335	SPEYCMDYH-IGLRADIKLYKMSWCKRYNVRN	367	
DB	320	SPEYIMDQDLQMPAVLKRKLRTAVYKRNQAVRN	453	
RESULT	6			
Q90063				
ID	Q90063	PRELIMINARY;	PRT: 274 AA.	
AC	Q90063;			
DT	01-MAY-2000 (PREMREL. 13, Created)			
DR	01-MAY-2000 (PREMREL. 13, Last sequence update)			
UF	01-MAY-2000 (PREMREL. 13, Last annotation update)			
DE	B(A)-SPECIFIC ALPHA 1->3 GALACTOSYLTRANSFERASE (FRAGMENT).			
GN	ABO.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
OX	NCBI_TaxID=9606;			
RN	(1)			
RA	SEQUENCE FROM N.A.			
RP	Yamamoto F.;			
RI	"Human histo-blood group ABO gene locus alleles."			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AF134433; AAD26583.1; ..			
DR	EMBL: AF134433; AAD26583.1; JOINED.			
KW	Transferase; glycosyltransferase.			
FT	NON_TER	1		
FT	NON_TER	274		
SO	SEQUENCE	274 AA; 31894 MW; 65f322EA024H473 C8C64;		
Query Match		33.5%	Score 671;	DB 4; Length 274;
Best Local Similarity		47.1%	Pred. No. 26-46;	
Matches 129;	Conservative 47;	Mismatches 96;	Indels 2;	Gaps 2;
QY	95	REPVATMDKAPRVWESTYKRAVLDDYAAKQITVGLITPAVAGKITEHYEEELTSANK	154	
DB	1	KKDYLVVPLALPIWSEPTFNIDINQFRLONTIGLITPAIKKYVA-FKLPLEAK	59	
QY	155	HEMVGHRYFYVMVDVSRMPLIELGPKSKFVEFKEREDRQVSNRMKILCEHVAH	214	
DB	60	HEMVGHRYHYFTDQLAAVPRVTLGTGQSLVLEPRAYKRDQVSHKIMELSPCTEK	119	
QY	215	IQREVDPLFCMDVDFODEPGEFTIGESVAQLQMWYKADPEFTYERKKESAAVIFEG	274	
DB	120	FLSEVDYLVCVDVDEPFDHVGVELLTPLFTLHPGFGSSSEATFYERPRQVAYIKD	179	
QY	275	EGDFYYHAALFEGTIPQVINITQESFKGLIKDKKDIFQAMQDSEHLNKFTLANKPTKL	334	
DB	180	EGDFYYLGGFGGSGVQEVQRLTRACHQAMVVDQANGIAVWHDSEHLNKYLLRHKPTKL	239	

Seq	Accession	Species	Length	Score	Pos	Gap
01	U00006.9	Human	274	4.48	670	4
02	U00006.9	Human	274	4.48	670	4
03	U00006.9	Human	274	4.48	670	4
04	U00006.9	Human	274	4.48	670	4
05	U00006.9	Human	274	4.48	670	4
06	U00006.9	Human	274	4.48	670	4
07	U00006.9	Human	274	4.48	670	4
08	U00006.9	Human	274	4.48	670	4
09	U00006.9	Human	274	4.48	670	4
10	U00006.9	Human	274	4.48	670	4
11	U00006.9	Human	274	4.48	670	4
12	U00006.9	Human	274	4.48	670	4
13	U00006.9	Human	274	4.48	670	4
14	U00006.9	Human	274	4.48	670	4
15	U00006.9	Human	274	4.48	670	4
16	U00006.9	Human	274	4.48	670	4
17	U00006.9	Human	274	4.48	670	4
18	U00006.9	Human	274	4.48	670	4
19	U00006.9	Human	274	4.48	670	4
20	U00006.9	Human	274	4.48	670	4
21	U00006.9	Human	274	4.48	670	4
22	U00006.9	Human	274	4.48	670	4
23	U00006.9	Human	274	4.48	670	4
24	U00006.9	Human	274	4.48	670	4
25	U00006.9	Human	274	4.48	670	4
26	U00006.9	Human	274	4.48	670	4
27	U00006.9	Human	274	4.48	670	4
28	U00006.9	Human	274	4.48	670	4
29	U00006.9	Human	274	4.48	670	4
30	U00006.9	Human	274	4.48	670	4
31	U00006.9	Human	274	4.48	670	4
32	U00006.9	Human	274	4.48	670	4
33	U00006.9	Human	274	4.48	670	4
34	U00006.9	Human	274	4.48	670	4
35	U00006.9	Human	274	4.48	670	4
36	U00006.9	Human	274	4.48	670	4
37	U00006.9	Human	274	4.48	670	4
38	U00006.9	Human	274	4.48	670	4
39	U00006.9	Human	274	4.48	670	4
40	U00006.9	Human	274	4.48	670	4
41	U00006.9	Human	274	4.48	670	4
42	U00006.9	Human	274	4.48	670	4
43	U00006.9	Human	274	4.48	670	4
44	U00006.9	Human	274	4.48	670	4
45	U00006.9	Human	274	4.48	670	4
46	U00006.9	Human	274	4.48	670	4
47	U00006.9	Human	274	4.48	670	4
48	U00006.9	Human	274	4.48	670	4
49	U00006.9	Human	274	4.48	670	4
50	U00006.9	Human	274	4.48	670	4
51	U00006.9	Human	274	4.48	670	4
52	U00006.9	Human	274	4.48	670	4
53	U00006.9	Human	274	4.48	670	4
54	U00006.9	Human	274	4.48	670	4
55	U00006.9	Human	274	4.48	670	4
56	U00006.9	Human	274	4.48	670	4
57	U00006.9	Human	274	4.48	670	4
58	U00006.9	Human	274	4.48	670	4
59	U00006.9	Human	274	4.48	670	4
60	U00006.9	Human	274	4.48	670	4
61	U00006.9	Human	274	4.48	670	4
62	U00006.9	Human	274	4.48	670	4
63	U00006.9	Human	274	4.48	670	4
64	U00006.9	Human	274	4.48	670	4

DE	01-MAY2000 (11EMBLref. 13, last annotation update)
DE	AI-SPECIFIC ALPHA 1-3-N-ACETYLGLUCOSAMINYLTRANSFERASE (PRAESENT)
CN	AAO.
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catartida; Hominoidea; Homo.
OX	NCBI_TaxId=9606;
KN	11
RP	SEQUENCE FROM N.A.
RA	Yamamoto F.;
RE	"Human histo-blood group Abo gene locus alleles."
RE	Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
ER	EMBL: AF134418; ADD26575.1; ..
ER	EMBL: AF134417; ADD26575.1; JOINED.
KW	transferase.
FT	NON_FER
FT	1
FT	274
FT	274
SEQUENCE	274 AA; 31961 MW; 1297144 CD; 953486 CPG64.

[illegible]

DI 01-MAY-2000 (TREMBLrel. 13, last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, last annotation update)
 DE ABO GLYCOSYLTRANSFERASE (FRAGMENT).
 GN MAMU_ABO.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecidae; Macaca.
 OX NCBI_TaxId=9544;
 RN 11
 RP SEQUENCE FROM N.A.
 RC STRAIN=RH427;
 RX MEDLINE=99409615; PubMed=10480696;
 RA Kernatrec N., Roubinet F., Apoll P.A., Blanchet A.;
 RT *Comparison of allele O sequences of the human and non-human primate
 AB system.*
 RL Immunogenetics 49:517-526(1999).
 DR EMBL: AF094693; AAD56308.1; -;
 DR EMBL: AF094692; AAD56308.1; JOINED.
 KW Transferase.
 FT NON_TER 1
 SQ SEQUENCE 274 AA: 31905 MW: 1038636615E5F8E6 CRC64;

Query Match 33.1%; Score 663; DB 6; Length 274;

Best Local Similarity 46.7%; Pred. No. 9e+46; Mismatches 98; Indels 2; Gaps 2;

DB 1 95 KREVVTIMKKAPVVECTYNRAVLDDYAKOKITVGLTFVAVGRYTEHYLEELTSANK 154
 1 KRDVLVTPMLAPVWEGTFNIDLNQFRLQNTTIGLTFVAKRYVA-FLKLFLETAEK 59
 QY 155 HEMVGRVLFYVWVDVSRMPLIEGLPSKFEVFEVKKPRRWQDVSMVRKTIQEHIVAH 214
 60 HEMVGRVRYVFTDQPAVPRVALQTRQLSYLGRVAYKRWQDVSMRMRMISDPCERR 119
 QY 215 LQREVPLECMQDVQVDFQDFGVLELIGESVADQAMWYKADPDFTYERKRESAAIPEG 274
 120 FLESEVDYLVCAVDMDKFRQVGVETLPLEGLHPAFVGSRRAPFYERRRPOSQAYIPKD 179
 QY 275 EQLFYFHAALFGSTPTQVINIQEFCFKILDKKNDIEAQMHDESHLNKYFLNKPTKIL 334
 180 EEDFYFMGAFRFGSVQVQRLTRACHQAMVQDANSTEAVWHDESHLNKYLRLHKPTKYL 239
 QY 335 SPEYCMQVH-TGLPADIKLWMSWQTEKYNVYN 367
 240 SPEYIMDOOLIGWPAVLRKLRFAVAPKRNQAVRN 273

Search completed: November 5, 2001, 15:22:20
 Job time: 8383 sec

